AMENDMENTS TO THE CLAIMS

This listing of the claims replaces all prior listings and versions:

1. (currently amended): A method for altering chromatin structure in a region of interest in chromosomal cellular chromatin, the method comprising the step of contacting the chromosomal cellular chromatin with a fusion molecule that binds to a binding site in the region of interest, wherein the fusion molecule comprises a DNA binding domain and at least one subunit protein of a chromatin remodeling complex or functional fragment of the subunit protein, wherein the contacting is conducted under conditions such that the structure of chromosomal chromatin is altered in the region of interest, and further wherein the altering facilitates access of a second molecule to cellular DNA ~~fusion molecule does not regulate transcription~~.

2. (original): The method of claim 1, wherein the cellular chromatin is present in a plant cell.

3. (original): The method of claim 1, wherein the cellular chromatin is present in an animal cell.

4. (original): The method of claim 3, wherein the cell is a human cell.

5. (previously presented): The method of claim 1, wherein the fusion molecule is a fusion polypeptide.

6. (original): The method of claim 1, wherein the DNA-binding domain comprises a zinc finger DNA-binding domain.

7. (withdrawn): The method of claim 1, wherein the DNA-binding domain is a triplex-forming nucleic acid or a minor groove binder.

8. (previously presented): The method of claim 1, wherein the subunit protein or functional fragment thereof acts as an enzyme.

9. (withdrawn): The method of claim 1, wherein the subunit protein or functional fragment thereof is non-enzymatic.

10. (previously presented): The method of claim 1, wherein the alteration of chromatin

structure facilitates detection of a sequence of interest within said chromatin.

11. (original): The method of claim 10, wherein the sequence of interest comprises a single nucleotide polymorphism.

12. (previously presented): The method of claim 1, wherein the alteration of chromatin structure facilitates activation of a gene of interest.

13. (previously presented): The method of claim 1, wherein the alteration of chromatin structure facilitates repression of a gene of interest.

14. (withdrawn) The method of claim 1, wherein chromatin modification facilitates recombination between an exogenous nucleic acid and cellular chromatin.

15. (withdrawn) The method of claim 5, wherein the method further comprises the step of contacting a cell with a polynucleotide encoding the fusion polypeptide, wherein the fusion polypeptide is expressed in the cell.

16. (withdrawn): The method of claim 1, further comprising the step of identifying an accessible region in the cellular chromatin, wherein the fusion molecule binds to a target site in the accessible region.

17. (original): The method of claim 1, wherein the region of interest comprises a gene.

18. (original): The method of claim 17, wherein the gene encodes a product selected from the group consisting of vascular endothelial growth factor, erythropoietin, androgen receptor, PPAR-γ2, p16, p53, pRb, dystrophin and e-cadherin.

19. (original): The method of claim 1, further comprising the step of contacting the cellular chromatin with a second molecule.

20. (original): The method of claim 19, wherein the second molecule is a transcriptional regulatory protein.

21. (original): The method of claim 19, wherein the second molecule is a fusion molecule.

22. (original): The method of claim 21, wherein the second molecule is a fusion

polypeptide.

23. (original): The method of claim 21, wherein the second molecule comprises a zinc finger DNA-binding domain.

24. (original): The method of claim 23, wherein the second molecule further comprises a transcriptional activation domain.

25. (original): The method of claim 23, wherein the second molecule further comprises a transcriptional repression domain.

26. (original): The method of claim 23, wherein the second molecule further comprises a polypeptide sequence selected from the group consisting of a histone acetyl transferase, a histone deacetylase, a functional fragment of a histone acetyl transferase, and a functional fragment of a histone deacetylase.

27. (original): The method of claim 19, further comprising the step of contacting the cellular chromatin with a third molecule.

28. (original): The method of claim 27, wherein the third molecule is a transcriptional regulatory protein.

29. (original): The method of claim 27,wherein the third molecule is a fusion molecule.

30. (original): The method of claim 29,wherein the third molecule is a fusion polypeptide.

31. (original): The method of claim 29, wherein the third molecule comprises a zinc finger DNA-binding domain.

32. (original): The method of claim 31, wherein the third molecule further comprises a transcriptional activation domain.

33. (original): The method of claim 31, wherein the third molecule further comprises a transcriptional repression domain.

34. (withdrawn): A fusion polypeptide comprising:

a) a DNA binding domain; and

b) a component of a chromatin remodeling complex or a functional fragment

thereof.

35. (withdrawn): The polypeptide of claim 34, wherein the DNA-binding domain is a zinc finger DNA binding domain.

36. (withdrawn): The polypeptide of claim 34, wherein the DNA binding domain binds to a target site in a gene encoding a product selected from the group consisting of vascular endothelial growth factor, erythropoietin, androgen receptor, PPAR-γ2, p16, p53, pRb, dystrophin and e-cadherin.

37. (withdrawn): The polypeptide of claim 34, wherein the component of a chromatin remodeling complex or functional fragment thereof is an enzymatic component.

38. (withdrawn): The polypeptide of claim 34, wherein the component of a chromatin remodeling complex or functional fragment thereof is a non-enzymatic component.

39. (withdrawn): The polypeptide of claim 37, wherein the enzymatic component of a chromatin remodeling complex or functional fragment thereof is selected from the group consisting of a SWI/SNF complex family member, an Mi-2 complex family member, an ISWI complex family member, a BRM family member, a BRG/BAF complex family member, a Mot-1 complex family member, a Chd-1 family member, a Chd-2 family member, a Chd-3 family member, a Chd-4 family member, a histone acetyl transferase and a histone deacetylase.

40. (withdrawn): A polynucleotide encoding the fusion polypeptide of claim 34.

41. (withdrawn): A cell comprising the fusion polypeptide of claim 34.

42. (withdrawn): A cell comprising the polynucleotide of claim 40.

43. (currently amended): A method for modulating expression of a gene, the method comprising the steps of:

a) contacting chromosomal cellular chromatin with a first fusion molecule that binds to a binding site in the chromosomal cellular chromatin, wherein the binding site is in the gene and wherein the first fusion molecule comprises a DNA-binding domain and at least one subunit protein of a chromatin remodeling complex or functional fragment of the subunit protein, wherein the contacting is conducted under conditions such that the structure of chromosomal chromatin is altered in ~~the~~ a region of interest and further wherein the ~~fusion molecule~~ altering

facilitates access of a second molecule comprising a DNA-binding domain to cellular DNA; and

b) further contacting the cellular chromatin with ~~a~~ the second molecule, wherein the second molecule ~~that~~ binds to a target site in the gene and modulates expression of the gene.

44. (original): The method of claim 43, wherein modulation comprises activation of expression of the gene.

45. (original): The method of claim 43, wherein modulation comprises repression of expression of the gene.

46. (original): The method of claim 43 wherein the DNA-binding domain of the first fusion molecule comprises a zinc finger DNA-binding domain.

47. (original): The method of claim 43 wherein the second molecule is a polypeptide.

48. (original): The method of claim 47 wherein the second molecule comprises a zinc finger DNA-binding domain.

49. (original): The method of claim 48, wherein the second molecule further comprises an activation domain.

50. (original): The method of claim 48, wherein the second molecule further comprises a repression domain.

51. (original): The method of claim 43 wherein the second molecule is a transcription factor.

52. (original): The method of claim 51 wherein the transcription factor is an exogenous molecule.

53. (original): The method of claim 51 wherein the transcription factor is an endogenous molecule.

54. (original): The method of claim 43 wherein the first fusion molecule and the second molecule each comprise a zinc finger DNA-binding domain.

55. (original): The method of claim 43 wherein a plurality of first fusion molecules is contacted with cellular chromatin, wherein each of the first fusion molecules binds to a distinct

binding site.

56. (original): The method of claim 43, wherein a plurality of second molecules is contacted with cellular chromatin, wherein each of the second molecules binds to a distinct target site.

57. (original): The method of claim 55 wherein at least one of the first fusion molecules comprises a zinc finger DNA-binding domain.

58. (original): The method of claim 56 wherein at least one of the second molecules comprises a zinc finger DNA-binding domain.

59. (original): The method of claim 43 wherein the expression of a plurality of genes is modulated.

60. (original): The method of claim 59 wherein a plurality of first fusion molecules is contacted with cellular chromatin, wherein each of the first fusion molecules binds to a distinct binding site.

61. (original): The method of claim 60 wherein at least one of the first fusion molecules is a zinc finger fusion polypeptide.

62. (original): The method of claim 59, wherein a plurality of second molecules is contacted with cellular chromatin, wherein each of the second molecules binds to a distinct binding site.

63. (original): The method of claim 62 wherein at least one of the second molecules is a zinc finger fusion polypeptide.

64. (previously presented): The method of claim 59 wherein the first fusion molecule binds to a shared binding site in two or more of the plurality of genes.

65. (original): The method of claim 64 wherein the first fusion molecule is a zinc finger fusion polypeptide.

66. (previously presented): The method of claim 59 wherein the second molecule binds to a shared target site in two or more of the plurality of genes.

67. (original): The method of claim 66 wherein the second molecule is a zinc finger fusion polypeptide.

68. (previously presented): The method of claim 1, wherein the alteration of chromatin structure results in the generation of an accessible region in the cellular chromatin.

69. (original): The method of claim 68, wherein generation of the accessible region facilitates binding of an exogenous molecule.

70. (original): The method of claim 69, wherein the exogenous molecule is selected from the group consisting of polypeptides, nucleic acids, small molecule therapeutics, minor groove binders, major groove binders and intercalators.

71. (withdrawn): A method for producing a fusion polypeptide, wherein the fusion polypeptide comprises a zinc finger DNA binding domain and a component of a chromatin remodeling complex or a functional fragment thereof, the method comprising the step of expressing the polynucleotide of claim 40 in a suitable host cell.

72. (withdrawn): A method for binding an exogenous molecule to a binding site, wherein the binding site is located within a region of interest in cellular chromatin, wherein the method comprises:

(a) contacting cellular chromatin with a fusion molecule that binds to a binding site in the region of interest, wherein the fusion molecule comprises a DNA binding domain and a component of a chromatin remodeling complex or functional fragment thereof, thereby modifying cellular chromatin within the region of interest; and

(b) introducing the exogenous molecule into the cell;

whereby the exogenous molecule binds to the binding site.